



ISU-003AX Seq

SEQUENCE LISTING

<110> Myers, Alan M.
James, Martha G.
<120> dull1 Coding for a Novel Starch Synthase and Uses
Thereof
<130> D6036PCT
<140> PCT/US98/24225
<141> 1998-11-12
<150> US 08/062,102
<151> 1997-11-12
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<223> cDNA sequence corresponding to the gene encoding the
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<210> 4
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<223> Primer_dul-sp4 used to amplify cloned BamHI fragment.
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site in the left arm in (gt11 phage DNA used to
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<400> 5
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<210> 6
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site in the LacZ' region in the right arm in (gt11
phage DNA used to amplify cDNA inserts.
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<223> Six residue M-box sequence in first half- repeat of ten
residue sequence of SBE-repeat in DU1.
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1 5

<210> 10
<211> 4
<212> PRT
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ten residue SBE-repeat sequence in DU1.
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<213> unknown
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<223> Deduced amino acid sequence of starch synthase DU1.
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Gly Pro Val Leu Ile Phe Arg Pro Thr Val Ala Gly Gly Gly Gly
20 25 30

Gly Thr Gln Ser Leu Leu Arg Thr Thr Arg Phe Ala Arg Arg Arg
35 40 45

Val Ile Arg Cys Val Val Ala Ser Pro Gly Cys Pro Asn Arg Lys
50 55 60

Ser Arg Thr Ala Ser Pro Asn Val Lys Val Ala Ala Tyr Ser Asn
65 70 75

Tyr Ala Pro Arg Leu Leu Val Glu Ser Ser Ser Lys Lys Ser Glu
80 85 90

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His His Asp Ser	Ser Arg His Arg	Glu Glu Thr Ile	Asp Thr Tyr	95	100	105
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Asp Val Glu Ile	Glu Val Asp Leu Gln	His Ile Ser Glu	Glu Glu	125	130	135
Leu Pro Gly Lys	Val Ser Ile Asn Ala	Ser Leu Gly Glu	Met Glu	140	145	150
Thr Val Asp Glu	Ala Glu Val Glu Glu	Asp Lys Phe Glu	Val Asp	155	160	165
Thr Ser Gly Ile	Val Leu Arg Asn Val	Ala Val Arg Glu	Val Asp	170	175	180
Pro Lys Asp Glu	His Asn Ala Lys Asp	Val Phe Val Val	Asp Ser	185	190	195
Ser Gly Thr Ala	Pro Asp Asn Ala Ala	Val Glu Glu Val	Val Asp	200	205	210
Glu Ala Glu Val	Glu Glu Asp Met Val	Asp Val Asp Ile	Leu Gly	215	220	225
Leu Asp Leu Asn	Asn Ala Thr Ile Glu	Glu Ile Asp Leu	Met Glu	230	235	240
Glu Ala Leu Leu	Glu Asn Phe Asp Val	Asp Ser Pro Gly	Asn Ala	245	250	255
Ser Ser Gly Arg	Thr Tyr Gly Gly Val	Asp Glu Leu Gly	Glu Leu	260	265	270
Pro Ser Thr Ser	Val Asp Cys Ile Ala	Ile Asn Gly Lys	Arg Arg	275	280	285
Ser Leu Lys Pro	Lys Pro Leu Pro Ile	Val Arg Phe Gln	Glu Gln	290	295	300
Glu Gln Ile Val	Leu Ser Ile Val Asp	Glu Glu Gly Leu	Ile Ala	305	310	315
Ser Ser Cys Glu	Glu Gly Gln Pro Val	Val Asp Tyr Asp	Lys Gln	320	325	330
Glu Glu Asn Ser	Thr Ala Phe Asp Glu	Gln Lys Gln Leu	Thr Asp	335	340	345
Asp Phe Pro Glu	Glu Gly Ile Ser Ile	Val His Phe Pro	Glu Pro	350	355	360
Asn Asn Asp Ile	Val Gly Ser Ser Lys	Phe Leu Glu Gln	Lys Gln	365	370	375
Glu Leu Asp Gly	Ser Tyr Lys Gln Asp	Arg Ser Thr Thr	Gly Leu	380	385	390
His Glu Gln Asp	Gln Ser Val Val Ser	Ser His Gly Gln	Asp Lys			

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Ser Ile Val Gly Val Pro Gln Gln Ile Gln Tyr Asn Asp Gln Ser	410	420
Ile Ala Gly Ser His Arg Gln Asp Gln Ser Ile Ala Gly Ala Pro	425	435
Glu Gln Ile Gln Ser Val Ala Gly Tyr Ile Lys Pro Asn Gln Ser	440	450
Ile Val Gly Ser Cys Lys Gln His Glu Leu Ile Ile Pro Glu Pro	455	465
Lys Lys Ile Glu Ser Ile Ile Ser Tyr Asn Glu Ile Asp Gln Ser	470	480
Ile Val Gly Ser His Lys Gln Asp Lys Ser Val Val Ser Val Pro	485	495
Glu Gln Ile Gln Ser Ile Val Ser His Ser Lys Pro Asn Gln Ser	500	510
Thr Val Asp Ser Tyr Arg Gln Ala Glu Ser Ile Ile Gly Val Pro	515	525
Glu Lys Val Gln Ser Ile Thr Ser Tyr Asp Lys Leu Asp Gln Ser	530	540
Ile Val Gly Ser Leu Lys Gln Asp Glu Pro Ile Ile Ser Val Pro	545	555
Glu Lys Ile Gln Ser Ile Val His Tyr Thr Lys Pro Asn Gln Ser	560	570
Ile Val Gly Leu Pro Lys Gln Gln Gln Ser Ile Val His Ile Val	575	585
Glu Pro Lys Gln Ser Ile Asp Gly Phe Pro Lys Gln Asp Leu Ser	590	600
Ile Val Gly Ile Ser Asn Glu Phe Gln Thr Lys Gln Leu Ala Thr	605	615
Val Gly Thr His Asp Gly Leu Leu Met Lys Gly Val Glu Ala Lys	620	630
Glu Thr Ser Gln Lys Thr Glu Gly Asp Thr Leu Gln Ala Thr Phe	635	645
Asn Val Asp Asn Leu Ser Gln Lys Gln Glu Gly Leu Thr Lys Glu	650	660
Ala Asp Glu Ile Thr Ile Ile Glu Lys Ile Asn Asp Glu Asp Leu	665	675
Val Met Ile Glu Glu Gln Lys Ser Ile Ala Met Asn Glu Glu Gln	680	690
Thr Ile Val Thr Glu Glu Asp Ile Pro Met Ala Lys Val Glu Ile	695	705
Gly Ile Asp Lys Ala Lys Phe Leu His Leu Leu Ser Glu Glu Glu		

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Met	Leu	Gln	Glu	Leu	Ala	Glu	Lys	Asn	Tyr	Ser	Leu	Gly	Asn	Lys
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Leu	Phe	Thr	Tyr	Pro	Asp	Val	Leu	Lys	Ala	Asp	Ser	Thr	Ile	Asp
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Val	Leu	Ile	Lys	Gly	Ala	Phe	Asn	Gly	Trp	Lys	Trp	Arg	Phe	Phe
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Thr	Glu	Lys	Leu	His	Lys	Ser	Glu	Leu	Ala	Gly	Asp	Trp	Trp	Cys
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Cys	Lys	Leu	Tyr	Ile	Pro	Lys	Gln	Ala	Tyr	Arg	Met	Asp	Phe	Val
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Phe	Phe	Asn	Gly	His	Thr	Val	Tyr	Glu	Asn	Asn	Asn	Asn	Asn	Asp
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Phe	Val	Ile	Gln	Ile	Glu	Ser	Thr	Met	Asp	Glu	Asn	Leu	Phe	Glu
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Asp Phe His Ala Thr Leu Pro Asn Asn Met Thr Glu Glu Glu Tyr		1055	1060	1065
Trp Met Glu Glu Glu Gln Arg Ile Tyr Thr Arg Leu Gln Gln Glu		1070	1075	1080
Arg Arg Glu Arg Glu Glu Ala Ile Lys Arg Lys Ala Glu Arg Asn		1085	1090	1095
Ala Lys Met Lys Ala Glu Met Lys Glu Lys Thr Met Arg Met Phe		1100	1105	1110
Leu Val Ser Gln Lys His Ile Val Tyr Thr Glu Pro Leu Glu Ile		1115	1120	1125
His Ala Gly Thr Thr Ile Asp Val Leu Tyr Asn Pro Ser Asn Thr		1130	1135	1140
Val Leu Thr Gly Lys Pro Glu Val Trp Phe Arg Cys Ser Phe Asn		1145	1150	1155
Arg Trp Met Tyr Pro Gly Gly Val Leu Pro Pro Gln Lys Met Val		1160	1165	1170
Gln Ala Glu Asn Gly Ser His Leu Lys Ala Thr Val Tyr Val Pro		1175	1180	1185
Arg Asp Ala Tyr Met Met Asp Phe Val Phe Ser Glu Ser Glu Glu		1190	1195	1200
Gly Gly Ile Tyr Asp Asn Arg Asn Gly Leu Asp Tyr His Ile Pro		1205	1210	1215
Val Phe Gly Ser Ile Ala Lys Glu Pro Pro Met His Ile Val His		1220	1225	1230
Ile Ala Val Glu Met Ala Pro Ile Ala Lys Val Gly Gly Leu Gly		1235	1240	1245
Asp Val Val Thr Ser Leu Ser Arg Ala Val Gln Asp Leu Gly His		1250	1255	1260
Asn Val Glu Val Ile Leu Pro Lys Tyr Gly Cys Leu Asn Leu Ser		1265	1270	1275
Asn Val Lys Asn Leu Gln Ile His Gln Ser Phe Ser Trp Gly Gly		1280	1285	1290
Ser Glu Ile Asn Val Trp Arg Gly Leu Val Glu Gly Leu Cys Val		1295	1300	1305
Tyr Phe Leu Glu Pro Gln Asn Gly Met Phe Gly Val Gly Tyr Val		1310	1315	1320
Tyr Gly Arg Asp Asp Asp Arg Arg Phe Gly Phe Phe Cys Arg Ser		1325	1330	1335

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Ala Leu Glu Phe Leu Leu Gln Ser Gly Ser Ser Pro Asn Ile Ile
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His Cys His Asp Trp Ser Ser Ala Pro Val Ala Trp Leu His Lys
 1355 1360 1365

Glu Asn Tyr Ala Lys Ser Ser Leu Ala Asn Ala Arg Val Val Phe
 1370 1375 1380

Thr Ile His Asn Leu Glu Phe Gly Ala His His Ile Gly Lys Ala
 1385 1390 1395

Met Arg Tyr Cys Asp Lys Ala Thr Thr Val Ser Asn Thr Tyr Ser
 1400 1405 1410

Lys Glu Val Ser Gly His Gly Ala Ile Val Pro His Leu Gly Lys
 1415 1420 1425

Phe Tyr Gly Ile Leu Asn Gly Ile Asp Pro Asp Ile Trp Asp Pro
 1430 1435 1440

Tyr Asn Asp Asn Phe Ile Pro Val His Tyr Thr Cys Glu Asn Val
 1445 1450 1455

Val Glu Gly Lys Arg Ala Ala Lys Arg Ala Leu Gln Gln Lys Phe
 1460 1465 1470

Gly Leu Gln Gln Ile Asp Val Pro Val Val Gly Ile Val Thr Arg
 1475 1480 1485

Leu Thr Ala Gln Lys Gly Ile His Leu Ile Lys His Ala Ile His
 1490 1495 1500

Arg Thr Leu Glu Arg Asn Gly Gln Val Val Leu Leu Gly Ser Ala
 1505 1510 1515

Pro Asp Ser Arg Ile Gln Ala Asp Phe Val Asn Leu Ala Asn Thr
 1520 1525 1530

Leu His Gly Val Asn His Gly Gln Val Arg Leu Ser Leu Thr Tyr
 1535 1540 1545

Asp Glu Pro Leu Ser His Leu Ile Tyr Ala Gly Ser Asp Phe Ile
 1550 1555 1560

Leu Val Pro Ser Ile Phe Glu Pro Cys Gly Leu Thr Gln Leu Val
 1565 1570 1575

Ala Met Arg Tyr Gly Thr Ile Pro Ile Val Arg Lys Thr Gly Gly
 1580 1585 1590

Leu Phe Asp Thr Val Phe Asp Val Asp Asn Asp Lys Glu Arg Ala
 1595 1600 1605

Arg Asp Arg Gly Leu Glu Pro Asn Gly Phe Ser Phe Asp Gly Ala
 1610 1615 1620

Asp Ser Asn Gly Val Asp Tyr Ala Leu Asn Arg Ala Ile Ser Ala
 1625 1630 1635

Trp Phe Asp Ala Arg Ser Trp Phe His Ser Leu Cys Lys Arg Val
 1640 1645 1650

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Met Glu Gln Asp Trp Ser Trp Asn Arg Pro Ala Leu Asp Tyr Ile
1655 1660 1665

Glu Leu Tyr Arg Ser Ala Ser Lys Leu
1670

<210> 13
<211> 60
<212> PRT
<213> maize
<220>
<221> 418..477
<222> REPEAT
<223> First 60 amino acid residue SBE-superrepeat of 180
amino acid repeat residue in DU1.
<400> 13

Asp Gln Ser Ile Ala Gly Ser His Arg Gln Asp Gln Ser Ile Ala
1 5 10 15

Gly Ala Pro Glu Gln Ile Gln Ser Val Ala Gly Tyr Ile Lys Pro
20 25 30

Asn Gln Ser Ile Val Gly Ser Cys Lys Gln His Glu Leu Ile Ile
35 40 45

Pro Glu Pro Lys Lys Ile Glu Ser Ile Ile Ser Tyr Asn Glu Ile
50 55 60

<210> 14
<211> 60
<212> PRT
<213> maize
<220>
<221> REPEAT
<221> 478..537
<223> Second 60 amino acid residue SBE-superrepeat of 180
amino acid repeat residue in DU1.
<400> 14

Asp Gln Ser Ile Val Gly Ser His Lys Gln Asp Lys Ser Val Val
1 5 10 15

Ser Val Pro Glu Gln Ile Gln Ser Ile Val Ser His Ser Lys Pro
20 25 30

Asn Gln Ser Thr Val Pro Ser Tyr Arg Gln Ala Glu Ser Ile Ile
35 40 45

Gly Val Pro Glu Lys Val Gln Ser Ile Thr Ser Tyr Asp Lys Leu
50 55 60

<210> 15
<211> 60
<212> PRT
<213> maize
<220>
<221> REPEAT
<221> 438..597
<223> Third 60 amino acid residue SBE-superrepeat of 180
amino acid repeat residue in DU1.
<400> 15

Asp Gln Ser Ile Val Gly Ser Leu Lys Gln Asp Glu Pro Ile Ile
1 5 10 15

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Ser Val Pro Glu Lys Ile Gln Ser Ile Val His Tyr Thr Lys Pro
20 25 30

Asn Gln Ser Ile Val Gly Leu Pro Lys Gln Gln Gln Ser Ile Val
35 40 45

His Ile Val Glu Pro Lys Gln Ser Ile Asp Gly Phe Pro Lys Gln
50 55 60

<210> 16
<211> 10
<212> PRT
<213> maize
<220>
<221> 478..487
<222> REPEAT
<223> Sequence of SBE-repeat in DU1.
<400> 16

Asp Gln Ser Ile Val Gly Ser His Lys Gln
1 5 10

<210> 17
<211> 10
<212> PRT
<213> maize
<220>
<221> 538..547
<222> REPEAT
<223> Sequence of SBE-repeat in DU1.
<400> 17

Asp Gln Ser Ile Val Gly Ser Leu Lys Gln
1 5 10

<210> 18
<211> 10
<212> PRT
<213> maize
<220>
<221> 448.457
<222> REPEAT
<223> Sequence of SBE-repeat in DU1.
<400> 18

Asn Gln Ser Ile Val Gly Ser Cys Lys Gln
1 5 10

<210> 19
<211> 10
<212> PRT
<213> maize
<220>
<221> 568..577
<222> REPEAT
<223> Sequence of SBE-repeat in DU1.
<400> 19

Asn Gln Ser Ile Val Gly Leu Pro Lys Gln
1 5 10

<210> 20
<211> 10
<212> PRT
<213> maize
<220>
<221> 418..427
<222> REPEAT
<223> Sequence of SBE-repeat in DU1.
<400> 20

Asp Gln Ser Ile Ala Gly Ser His Arg Gln

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1          5          10
      <210> 21
      <211> 10
      <212> PRT
      <213> maize
      <220>
      <221> 428..437
      <222> REPEAT
      <223> Sequence of SBE-repeat in DU1.
      <400> 21
Asp Gln Ser Ile Ala Gly Ala Pro Glu Gln
1          5          10

      <210> 22
      <211> 10
      <212> PRT
      <213> maize
      <220>
      <221> 404..413
      <222> REPEAT
      <223> Sequence of SBE-repeat in DU1.
      <400> 22
Asp Lys Ser Ile Val Gly Val Pro Gln Gln
1          5          10

      <210> 23
      <211> 10
      <212> PRT
      <213> maize
      <220>
      <221> 598..607
      <222> REPEAT
      <223> Sequence of SBE-repeat in DU1.
      <400> 23
Asp Leu Ser Ile Val Gly Asn Glu Phe Gln
1          5          10

      <210> 24
      <211> 25
      <212> PRT
      <213> maize
      <220>
      <221> 529..553
      <222> REPEAT
      <223> Conserved M-box sequence in maize SBEI.
      <400> 24
Lys Cys Ile Ala Tyr Ala Glu Ser His Asp Gln Ser Ile Val Gly
1          5          10          15

Asp Lys Thr Ile Ala Phe Leu Leu Met Asp
          20          25

      <210> 25
      <211> 25
      <212> PRT
      <213> pea
      <220>
      <221> 529..553
      <222> REPEAT
      <223> Conserved M-box sequence in pea SBEII.
      <400> 25
Lys Cys Val Ser Tyr Ala Glu Ser His Asp Gln Ser Ile Val Gly
1          5          10          15

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Asp Lys Thr Ile Ala Phe Leu Leu Met Asp
20 25

<210> 26
<211> 25
<212> PRT
<213> wheat
<220>
<221> 529..553
<222> REPEAT
<223> Conserved M-box sequence in wheat SBEI.
<400> 26

Lys Cys Ile Ala Tyr Ala Glu Ser His Asp Gln Ser Ile Val Gly
1 5 10 15

Asp Lys Thr Met Ala Phe Leu Leu Met Asp
20 25

<210> 27
<211> 25
<212> PRT
<213> maize
<220>
<221> 572..596
<222> REPEAT
<223> Conserved M-box sequence in maize SBEIa.
<400> 27

Lys Cys Val Thr Tyr Cys Glu Ser His Asp Gln Ala Leu Val Gly
1 5 10 15

Asp Lys Thr Ile Ala Phe Trp Leu Met Asp
20 25

<210> 28
<211> 15
<212> PRT
<213> maize
<220>
<221> 572..596
<222> REPEAT
<223> Conserved M-box sequence in maize SBEIIb.
<400> 28

Lys Cys Val Thr Tyr Ala Glu Ser His Asp Gln Ala Leu Val Gly
1 5 10 15

<210> 29
<211> 25
<212> PRT
<213> pea
<220>
<221> 572..596
<222> REPEAT
<223> Conserved M-box sequence in pea SBEI.
<400> 29

Lys Cys Val Val Tyr Cys Glu Ser His Asp Gln Ala Leu Val Gly
1 5 10 15

Asp Lys Thr Met Ala Phe Leu Leu Met Asp
20 25

<210> 30
<211> 25
<212> PRT
<213> yeast

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<220>
<221> 477..501
<222> REPEAT
<223> Conserved M-box sequence in yeast GLC3 glycogen
        synthase.
<400> 30
Lys Val Val Ala Tyr Cys Glu Ser His Asp Gln Ala Leu Val Gly
 1      5      10      15
Asp Lys Ser Leu Ala Phe Trp Leu Met Asp
        20      25

<210> 31
<211> 25
<212> PRT
<213> Homo sapiens
<220>
<221> 477..501
<222> REPEAT
<223> Conserved M-box sequence in human liver glycogen
        synthase.
<400> 31
Lys Cys Ile Ala Tyr Ala Glu Ser His Asp Gln Ala Leu Val Gly
 1      5      10      15
Asp Lys Thr Leu Ala Phe Trp Leu Met Asp
        20      25

<210> 32
<211> 28
<212> PRT
<213> maize
<220>
<221> 150..177
<222> REPEAT
<223> Second 28 amino acid residue repeat of 85 residue
        repeat in N-terminus of DU1.
<400> 32
Glu Thr Val Asp Glu Ala Glu Val Glu Glu Asp Lys Phe Glu Val
 1      5      10      15
Asp Thr Ser Gly Ile Val Leu Arg Asn Val Ala Val Arg
        20      25

<210> 33
<211> 29
<212> PRT
<213> artificial sequence
<220>
<221> 178..205
<222> REPEAT
<223> Second 28 amino acid residue repeat of 85 residue
        repeat in N-terminus of DU1.
<400> 33
Glu Val Asp Pro Lys Asp Glu His Asn Ala Lys Asp Val Phe Val
 1      5      10      15
Val Asp Ser Ser Gly Thr Ala Pro Asp Asn Ala Ala Val Glu
        20      25

<210> 34
<211> 27
<212> PRT
<213> maize
<220>

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<221> 206..233

<222> REPEAT

<223> Third 28 amino acid residue repeat of 85 residue repeat in N-terminus of DU1.

<400> 34

Glu	Val	Val	Asp	Glu	Ala	Glu	Val	Glu	Glu	Asp	Met	Val	Asp	Val
1				5					10					15

Asp	Ile	Leu	Gly	Leu	Asp	Leu	Asn	Asn	Ala	Thr	Ile
				20					25		

<210> 35

<211> 1230

<212> PRT

<213> potato

<220>

<223> Deduced amino acid sequence of potato starch synthase SSIII.

<400> 35

Met	Asp	Val	Pro	Phe	Pro	Leu	His	Arg	Ser	Leu	Ser	Cys	Thr	Ser
1				5					10					15
Val	Ser	Asn	Ala	Ile	Thr	His	Leu	Lys	Ile	Lys	Pro	Ile	Leu	Gly
				20					25					30

Phe	Val	Ser	His	Gly	Thr	Thr	Ser	Leu	Ser	Val	Gln	Ser	Ser	Ser
				35					40					45

Trp	Arg	Lys	Asp	Gly	Met	Val	Thr	Gly	Val	Ser	Phe	Ser	Ile	Cys
				50					55					60

Ala	Asn	Phe	Ser	Gly	Arg	Arg	Arg	Arg	Lys	Val	Ser	Thr	Pro	Arg
				65					70					75

Ser	Gln	Gly	Ser	Ser	Pro	Lys	Gly	Phe	Val	Pro	Arg	Lys	Pro	Ser
				80					85					90

Gly	Met	Ser	Thr	Gln	Arg	Lys	Val	Gln	Lys	Ser	Asn	Gly	Asp	Lys
				95					100					105

Glu	Ser	Lys	Ser	Thr	Ser	Thr	Ser	Lys	Glu	Ser	Glu	Ile	Ser	Asn
				110					115					120

Gln	Lys	Thr	Val	Glu	Ala	Arg	Val	Glu	Thr	Ser	Asp	Asp	Asp	Thr
				125					130					135

Lys	Gly	Val	Val	Arg	Asp	His	Lys	Phe	Leu	Glu	Asp	Glu	Asp	Glu
				140					145					150

Ile	Asn	Gly	Ser	Thr	Lys	Ser	Ile	Ser	Met	Ser	Pro	Val	Arg	Val
				155					160					165

Ser	Ser	Gln	Phe	Val	Glu	Ser	Glu	Glu	Thr	Gly	Gly	Asp	Asp	Lys
				170					175					180

Asp	Ala	Val	Lys	Leu	Asn	Lys	Ser	Lys	Arg	Ser	Glu	Glu	Ser	Gly
				185					190					195

Phe	Ile	Ile	Asp	Ser	Val	Ile	Arg	Glu	Gln	Ser	Gly	Ser	Gln	Gly
				200					205					210

Glu	Thr	Asn	Ala	Ser	Ser	Lys	Gly	Ser	His	Ala	Val	Gly	Thr	Lys
				215					220					225

Leu	Tyr	Glu	Ile	Leu	Gln	Val	Asp	Val	Glu	Pro	Gln	Gln	Leu	Lys

230 235 240

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545	550	555
Val Lys Lys Leu	Val Lys Ser Glu Arg	Ile Asp Gly Asp Trp Trp
560	565	570
Tyr Thr Glu Val	Val Ile Pro Asp Gln	Ala Leu Phe Leu Asp Trp
575	580	585
Val Phe Ala Asp	Gly Pro Pro Lys His	Ala Ile Ala Tyr Asp Asn
590	595	600
Asn His Arg Gln	Asp Phe His Ala Ile	Val Pro Asn His Ile Pro
605	610	615
Glu Glu Leu Tyr	Trp Val Glu Glu Glu	His Gln Ile Phe Lys Thr
620	625	630
Leu Gln Glu Glu	Arg Arg Leu Arg Glu	Ala Ala Met Arg Ala Lys
635	640	645
Val Glu Lys Thr	Ala Leu Leu Lys Thr	Glu Thr Lys Glu Arg Thr
650	655	660
Met Lys Ser Phe	Leu Leu Ser Gln Lys	His Val Val Tyr Thr Glu
665	670	675
Pro Leu Asp Ile	Gln Ala Gly Ser Ser	Val Thr Val Tyr Tyr Asn
680	685	690
Pro Ala Asn Thr	Val Leu Asn Gly Lys	Pro Glu Ile Trp Phe Arg
695	700	705
Cys Ser Phe Asn	Arg Trp Thr His Arg	Leu Gly Pro Leu Pro Pro
710	715	720
Gln Lys Met Ser	Pro Ala Glu Asn Gly	Thr His Val Arg Ala Thr
725	730	735
Val Lys Val Pro	Leu Asp Ala Tyr Met	Met Asp Phe Val Phe Ser
740	745	750
Glu Arg Glu Asp	Gly Gly Ile Phe Asp	Asn Lys Ser Gly Met Asp
755	760	765
Tyr His Ile Pro	Val Phe Gly Gly Val	Ala Lys Glu Pro Pro Met
770	775	780
His Ile Val His	Ile Ala Val Glu Met	Ala Pro Ile Ala Lys Val
785	790	795
Gly Gly Leu Gly	Asp Val Val Thr Ser	Leu Ser Arg Ala Val Gln
800	805	810
Asp Leu Asn His	Asn Val Asp Ile Ile	Leu Pro Lys Tyr Asp Cys
815	820	825
Leu Lys Met Asn	Asn Val Lys Asp Phe	Arg Phe His Lys Asn Tyr
830	835	840
Phe Trp Gly Gly	Thr Glu Ile Lys Val	Trp Phe Gly Lys Val Glu
845	850	855

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Gly	Leu	Ser	Val	Tyr	Phe	Leu	Glu	Pro	Gln	Asn	Gly	Leu	Phe	Ser	860	865	870
Lys	Gly	Cys	Val	Tyr	Gly	Cys	Ser	Asn	Asp	Gly	Glu	Arg	Phe	Gly	875	880	885
Phe	Phe	Cys	His	Ala	Ala	Leu	Glu	Phe	Leu	Leu	Gln	Gly	Gly	Phe	890	895	900
Ser	Pro	Asp	Ile	Ile	His	Cys	His	Asp	Trp	Ser	Ser	Ala	Pro	Val	905	910	915
Ala	Trp	Leu	Phe	Lys	Glu	Gln	Tyr	Thr	His	Tyr	Gly	Leu	Ser	Lys	920	925	930
Ser	Arg	Ile	Val	Phe	Thr	Ile	His	Asn	Leu	Glu	Phe	Gly	Ala	Asp	935	940	945
Leu	Ile	Gly	Arg	Ala	Met	Thr	Asn	Ala	Asp	Lys	Ala	Thr	Thr	Val	950	955	960
Ser	Pro	Thr	Tyr	Ser	Gln	Glu	Val	Ser	Gly	Asn	Pro	Val	Ile	Ala	965	970	975
Pro	His	Leu	His	Lys	Phe	His	Gly	Ile	Val	Asn	Gly	Ile	Asp	Pro	980	985	990
Asp	Ile	Trp	Asp	Pro	Leu	Asn	Asp	Lys	Phe	Ile	Pro	Ile	Pro	Tyr	995	1000	1005
Thr	Ser	Glu	Asn	Val	Val	Glu	Gly	Lys	Thr	Ala	Ala	Lys	Glu	Ala	1010	1015	1020
Leu	Gln	Arg	Lys	Leu	Gly	Leu	Lys	Gln	Ala	Asp	Leu	Pro	Leu	Val	1025	1030	1035
Gly	Ile	Ile	Thr	Arg	Leu	Thr	His	Gln	Lys	Gly	Ile	His	Leu	Ile	1040	1045	1050
Lys	His	Ala	Ile	Trp	Arg	Thr	Leu	Glu	Arg	Asn	Gly	Gln	Val	Val	1055	1060	1065
Leu	Leu	Gly	Ser	Ala	Pro	Asp	Pro	Arg	Val	Gln	Asn	Asn	Phe	Val	1070	1075	1080
Asn	Leu	Ala	Asn	Gln	Leu	His	Ser	Lys	Tyr	Asn	Asp	Arg	Ala	Arg	1085	1090	1095
Leu	Cys	Leu	Thr	Tyr	Asp	Glu	Pro	Leu	Ser	His	Leu	Ile	Tyr	Ala	1100	1105	1110
Gly	Ala	Asp	Phe	Ile	Leu	Val	Pro	Ser	Ile	Phe	Glu	Pro	Cys	Gly	1115	1120	1125
Leu	Thr	Gln	Leu	Thr	Ala	Met	Arg	Tyr	Gly	Ser	Ile	Pro	Val	Val	1130	1135	1140
Arg	Lys	Thr	Gly	Gly	Leu	Tyr	Asp	Thr	Val	Phe	Asp	Val	Asp	His	1145	1150	1155
Asp	Lys	Glu	Arg	Ala	Gln	Gln	Cys	Gly	Leu	Glu	Pro	Asn	Gly	Phe	1160	1165	1170

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Ser	Phe	Asp	Gly	Ala	Asp	Ala	Gly	Gly	Val	Asp	Tyr	Ala	Leu	Asn
			1175						1180					1185
Arg	Ala	Leu	Ser	Ala	Trp	Tyr	Asp	Gly	Arg	Asp	Trp	Phe	Asn	Ser
			1190						1195					1200
Leu	Cys	Lys	Gln	Val	Met	Glu	Gln	Asp	Trp	Ser	Trp	Asn	Arg	Pro
			1205						1210					1215
Ala	Leu	Asp	Tyr	Leu	Glu	Leu	Tyr	His	Ala	Ala	Arg	Lys	Leu	Glu
			1220						1225					1230

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 <212> DNA
 <213> artificial sequence
 <220>
 <222> repeat_unit
 <223> Sequence of the nine base pair direct repeats flanking
 a Mu1 element in cloned fragment.
 <400> 36

gtgagaatg 9

<210> 37
 <211> 32
 <212> DNA
 <213> artificial sequence
 <221> primer
 <223> Primer containing restriction sites
 <400> 37

aaacccgggaattcgatggagatgggtcctacg

32